

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/028,946

DATE: 01/15/2002

TIME: 15:28:59

Input Set : A:\LEX-0289-USA SEQLIST.txt

Output Set: N:\CRF3\01152002\J028946.raw

ENTERED

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4 <110> APPLICANT: Yu, Xuanchuan
5     Miranda, Maricar
6     Friddle, Carl Johan
8 <120> TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
10 <130> FILE REFERENCE: LEX-0289-USA
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/028,946
C--> 12 <141> CURRENT FILING DATE: 2001-12-20
12 <150> PRIOR APPLICATION NUMBER: US 60/258,335
13 <151> PRIOR FILING DATE: 2000-12-27
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17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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21 <212> TYPE: DNA
22 <213> ORGANISM: homo sapiens
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27 cagcagatgt ctctcttttc ccgagaaggg atattagatg ccctctttgt tctctttgaa      180
28 gaatgcagtc agcctgctct gatgaagatt aagcacgtga gcaactttgt ccggaagtat      240
29 tccgacacca tagctgagtt acaggagctc cagccttcgg caaaggactt cgaagtcaga      300
30 agtctttagt gttgtggtca ctttgotgaa gtgcagggtg taagagagaa agcaaccggg      360
31 gacatctatg ctatgaaagt gatgaagaag aaggctttat tggcccagga gcaggtttca      420
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34 gacttgctgt cacttttgaa tagatatgag gaccagttag atgaaaacct gatcacgttt      600
35 tacctagctg agctgatttt ggctgttcac agcgttcac tcatgggata cgtgcacoga      660
36 gacatcaagc ctgagaacat tctcgttgac cgcacaggac acatcaagct ggtggatttt      720
37 ggatctgccc cgaaaatgaa ttcaaacaa aggttgaatg ccaaaactcc gattgggacc      780
38 ccagattaca tggctcctga agtgcctgac gtgatgaacg gggatggaaa aggcacctac      840
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41 tttttgaaat ttccagatga ccccaaagtg agcagtgact ttcttgatct gattcaaagg      1020
42 ttgttgtgcg gccagaaaga gagactgaag tttgaaggtc tttgctgcc tcttttcttc      1080
43 tctaaaattg actggaacaa cattcgtaac tctctctccc ccttcgttcc caccctcaag      1140
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53 gtggaagaaa tgaggttgat gatgaatcag ttggaagagg atcttgtctc agcaagaaga      1740
54 cggagtgatc tctacgaatc tgagctgaga gagtctcggc ttgctgctga aqaattcaag      1800
55 cggaaagcga cagaatgtca gcataaactg ttgaaggcta aggatcaagg gaagcctgaa      1860

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58	aatatccgcc	aggcaaagga	gcgagccgag	agggagctgg	agaagctgca	gaaccgagag	2040
59	gattcttctg	aaggcatcag	aaagaagctg	gtggaagctg	aggaaacgag	ccattctctg	2100
60	gagaacaagg	taaagagact	agagaccatg	gagcgtagag	aaaacagact	gaaggatgac	2160
61	atccagacaa	aatcccaaca	gatccagcag	atygctgata	aaattctyga	gctcgaagag	2220
62	aaacatcggg	aggcccaagt	ctcagccag	caactagaag	tgcacctgaa	acagaaagag	2280
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68	ctggagacac	aggctgggaa	gttggaggcc	cagaaccgaa	aactggagga	gcagctggag	2640
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70	cgggaggtca	gtctagagca	cgaggagcag	aaactggagc	tcaagcgcca	gtccacagag	2760
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73	gaagaggaga	tccaggcaat	cacggcacat	agagatgaaa	tccagcgcaa	atttgatgct	2940
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79	aaagagcggc	agtgggaggc	ctggaggagc	gtcctgggtg	atgagaaatc	ccagtttgag	3300
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133 <212> TYPE: PRT
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139 Ala Glu Pro Ile Ala Ser Arg Ala Ser Arg Leu Asn Leu Phe Phe Gln
140 20 25 30
141 Gly Lys Pro Pro Phe Met Thr Gln Gln Met Ser Pro Leu Ser Arg
142 35 40 45
143 Glu Gly Ile Leu Asp Ala Leu Phe Val Leu Phe Glu Glu Cys Ser Gln
144 50 55 60
145 Pro Ala Leu Met Lys Ile Lys His Val Ser Asn Phe Val Arg Lys Tyr
146 65 70 75 80
147 Ser Asp Thr Ile Ala Glu Leu Gln Glu Leu Gln Pro Ser Ala Lys Asp
148 85 90 95
149 Phe Glu Val Arg Ser Leu Val Gly Cys Gly His Phe Ala Glu Val Gln
150 100 105 110
151 Val Val Arg Glu Lys Ala Thr Gly Asp Ile Tyr Ala Met Lys Val Met
152 115 120 125
153 Lys Lys Lys Ala Leu Leu Ala Gln Glu Gln Val Ser Phe Phe Glu Glu
154 130 135 140
155 Glu Arg Asn Ile Leu Ser Arg Ser Thr Ser Pro Trp Ile Pro Gln Leu
156 145 150 155 160
157 Gln Tyr Ala Phe Gln Asp Lys Asn His Leu Tyr Leu Val Met Glu Tyr

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159 Gln Pro Gly Gly Asp Leu Leu Ser Leu Leu Asn Arg Tyr Glu Asp Gln
160                               180                               185                               190
161 Leu Asp Glu Asn Leu Ile Gln Phe Tyr Leu Ala Glu Leu Ile Leu Ala
162                               195                               200                               205
163 Val His Ser Val His Leu Met Gly Tyr Val His Arg Asp Ile Lys Pro
164                               210                               215                               220
165 Glu Asn Ile Leu Val Asp Arg Thr Gly His Ile Lys Leu Val Asp Phe
166 225                               230                               235                               240
167 Gly Ser Ala Ala Lys Met Asn Ser Asn Lys Met Val Asn Ala Lys Leu
168                               245                               250                               255
169 Pro Ile Gly Thr Pro Asp Tyr Met Ala Pro Glu Val Leu Thr Val Met
170                               260                               265                               270
171 Asn Gly Asp Gly Lys Gly Thr Tyr Gly Leu Asp Cys Asp Trp Trp Ser
172                               275                               280                               285
173 Val Gly Val Ile Ala Tyr Glu Met Ile Tyr Gly Arg Ser Pro Phe Ala
174                               290                               295                               300
175 Glu Gly Thr Ser Ala Arg Thr Phe Asn Asn Ile Met Asn Phe Gln Arg
176 305                               310                               315                               320
177 Phe Leu Lys Phe Pro Asp Asp Pro Lys Val Ser Ser Asp Phe Leu Asp
178                               325                               330                               335
179 Leu Ile Gln Ser Leu Leu Cys Gly Gln Lys Glu Arg Leu Lys Phe Glu
180                               340                               345                               350
181 Gly Leu Cys Cys His Pro Phe Phe Ser Lys Ile Asp Trp Asn Asn Ile
182                               355                               360                               365
183 Arg Asn Ser Pro Pro Pro Phe Val Pro Thr Leu Lys Ser Asp Asp Asp
184                               370                               375                               380
185 Thr Ser Asn Phe Asp Glu Pro Glu Lys Asn Ser Trp Val Ser Ser Ser
186 385                               390                               395                               400
187 Pro Cys Gln Leu Ser Pro Ser Gly Phe Ser Gly Glu Glu Leu Pro Phe
188                               405                               410                               415
189 Val Gly Phe Ser Tyr Ser Lys Ala Leu Gly Ile Leu Gly Arg Ser Glu
190                               420                               425                               430
191 Ser Val Val Ser Gly Leu Asp Ser Pro Ala Lys Thr Ser Ser Met Glu
192                               435                               440                               445
193 Lys Lys Leu Leu Ile Lys Ser Lys Glu Leu Gln Asp Ser Gln Asp Lys
194                               450                               455                               460
195 Cys His Lys Met Glu Gln Glu Met Thr Arg Leu His Arg Arg Val Ser
196 465                               470                               475                               480
197 Glu Val Glu Ala Val Leu Ser Gln Lys Glu Val Glu Leu Lys Ala Ser
198                               485                               490                               495
199 Glu Thr Gln Arg Ser Leu Leu Glu Gln Asp Leu Ala Thr Tyr Ile Thr
200                               500                               505                               510
201 Glu Cys Ser Ser Leu Lys Arg Ser Leu Glu Gln Ala Arg Met Glu Val
202                               515                               520                               525
203 Ser Gln Glu Asp Asp Lys Ala Leu Gln Leu Leu His Asp Ile Arg Glu
204                               530                               535                               540
205 Gln Ser Arg Lys Leu Gln Glu Ile Lys Glu Gln Glu Tyr Gln Ala Gln
206 545                               550                               555                               560

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207 Val Glu Glu Met Arg Leu Met Met Asn Gln Leu Glu Glu Asp Leu Val
208           565           570           575
209 Ser Ala Arg Arg Arg Ser Asp Leu Tyr Glu Ser Glu Leu Arg Glu Ser
210           580           585           590
211 Arg Leu Ala Ala Glu Glu Phe Lys Arg Lys Ala Thr Glu Cys Gln His
212           595           600           605
213 Lys Leu Leu Lys Ala Lys Asp Gln Gly Lys Pro Glu Val Gly Glu Tyr
214           610           615           620
215 Ala Lys Leu Glu Lys Ile Asn Ala Glu Gln Gln Leu Lys Ile Gln Glu
216 625           630           635           640
217 Leu Gln Glu Lys Leu Glu Lys Ala Val Lys Ala Ser Thr Glu Ala Thr
218           645           650           655
219 Glu Leu Leu Gln Asn Ile Arg Gln Ala Lys Glu Arg Ala Glu Arg Glu
220           660           665           670
221 Leu Glu Lys Leu Gln Asn Arg Glu Asp Ser Ser Glu Gly Ile Arg Lys
222           675           680           685
223 Lys Leu Val Glu Ala Glu Glu Arg Arg His Ser Leu Glu Asn Lys Val
224 690           695           700
225 Lys Arg Leu Glu Thr Met Glu Arg Arg Glu Asn Arg Leu Lys Asp Asp
226 705           710           715           720
227 Ile Gln Thr Lys Ser Gln Gln Ile Gln Gln Met Ala Asp Lys Ile Leu
228           725           730           735
229 Glu Leu Glu Glu Lys His Arg Glu Ala Gln Val Ser Ala Gln His Leu
230           740           745           750
231 Glu Val His Leu Lys Gln Lys Glu Gln His Tyr Glu Glu Lys Ile Lys
232           755           760           765
233 Val Leu Asp Asn Gln Ile Lys Lys Asp Leu Ala Asp Lys Glu Thr Leu
234 770           775           780
235 Glu Asn Met Met Gln Arg His Glu Glu Glu Ala His Glu Lys Gly Lys
236 785           790           795           800
237 Ile Leu Ser Glu Gln Lys Ala Met Ile Asn Ala Met Asp Ser Lys Ile
238           805           810           815
239 Arg Ser Leu Glu Gln Arg Ile Val Glu Leu Ser Glu Ala Asn Lys Leu
240           820           825           830
241 Ala Ala Asn Ser Ser Leu Phe Thr Gln Arg Asn Met Lys Ala Gln Glu
242           835           840           845
243 Glu Met Ile Ser Glu Leu Arg Gln Gln Lys Phe Tyr Leu Glu Thr Gln
244           850           855           860
245 Ala Gly Lys Leu Glu Ala Gln Asn Arg Lys Leu Glu Glu Gln Leu Glu
246 865           870           875           880
247 Lys Ile Ser His Gln Asp His Ser Asp Lys Asn Arg Leu Leu Glu Leu
248           885           890           895
249 Glu Thr Arg Leu Arg Glu Val Ser Leu Glu His Glu Glu Gln Lys Leu
250           900           905           910
251 Glu Leu Lys Arg Gln Leu Thr Glu Leu Gln Leu Ser Leu Gln Glu Arg
252           915           920           925
253 Glu Ser Gln Leu Thr Ala Leu Gln Ala Ala Arg Ala Ala Leu Glu Ser
254 930           935           940
255 Gln Leu Arg Gln Ala Lys Thr Glu Leu Glu Glu Thr Thr Ala Glu Ala

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VERIFICATION SUMMARY

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Input Set : A:\LEX-0289-USA SEQLIST.txt

Output Set: N:\CRF3\01152002\J028946.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date